



PATENT  
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : DeBonte et al. Art Unit: 1804  
Serial No.: 08/572,027 Examiner: G. Benzion  
Filed : 12/14/95  
Title : PLANTS HAVING MUTANT SEQUENCES THAT CONFER ALTERED  
FATTY ACID PROFILES

Assistant Commissioner for Patents  
Washington, DC 20231

STATEMENT UNDER 37 CFR §1.825(b)

I hereby submit that the content of the substitute paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same and that the sequence listings contain no new matter.

Respectfully submitted,

Date: September 12, 1997

  
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10428.M11

Date of Deposit September 12, 1997  
I hereby certify under 37 CFR 1.8(a) that this correspondence is being deposited with the United States Postal Service as **first class mail** with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

  
Fish & Richardson  
10428.M11

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: DeBonte, L. et al.

(ii) TITLE OF INVENTION: PLANTS HAVING MUTANT SEQUENCES THAT CONFER  
ALTERED FATTY ACID PROFILES

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Minneapolis  
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(E) COUNTRY: USA  
(F) ZIP: 55402

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM compatible  
(C) OPERATING SYSTEM: Windows95  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/572,027  
(B) FILING DATE: 14-DEC-1995  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/416,497  
(B) FILING DATE: 04-APR-1995  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/170,886  
(B) FILING DATE: 21-DEC-1993  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/739,965  
(B) FILING DATE: 05-AUG-1991  
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/575,542  
(B) FILING DATE: 30-AUG-1990  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ellinger, Mark S.  
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(C) REFERENCE/DOCKET NUMBER: A21-535.10

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 612/335-5070  
(B) TELEFAX: 612/288-9696

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1155 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Brassica napus*

(ix) FEATURE:

(D) OTHER INFORMATION: Wild type F form.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|   |     |
|---|-----|
| ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT | 48  |
| Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser |     |
| 1 5 10 15   |     |
| GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT | 96  |
| Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr |     |
| 20 25 30  |     |
| GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG | 144 |
| Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser |     |
| 35 40 45  |     |
| ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC | 192 |
| Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser |     |
| 50 55 60  |     |
| TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT | 240 |
| Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro |     |
| 65 70 75 80   |     |
| CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC | 288 |
| Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val |     |
| 85 90 95  |     |
| CTA ACC GGC GTC TGG GTC ATA GCC CAC GAA TGC GGC CAC CAC GCC TTC | 336 |
| Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe |     |
| 100 105 110   |     |
| AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC | 384 |
| Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser |     |
| 115 120 125   |     |
| TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC | 432 |
| Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His |     |
| 130 135 140   |     |
| CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG | 480 |
| His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys |     |
| 145 150 155 160   |     |

|   |      |
|---|------|
| AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG<br>Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu<br>165 170 175     | 528  |
| GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG<br>Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu<br>180 185 190     | 576  |
| TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT<br>Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg<br>195 200 205     | 624  |
| TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC<br>Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu<br>210 215 220     | 672  |
| CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC<br>Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu<br>225 230 235 240 | 720  |
| TTC CGT TAC GCC GCC GGC CAG GGA GTG GCC TCG ATG GTC TGC TTC TAC<br>Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr<br>245 250 255     | 768  |
| GGA GTC CCG CTT CTG ATT GTC AAT GGT TTC CTC GTG TTG ATC ACT TAC<br>Gly Val Pro Leu Leu Val Asn Gly Phe Leu Val Leu Ile Thr Tyr<br>260 265 270         | 816  |
| TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG<br>Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp<br>275 280 285     | 864  |
| GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC<br>Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile<br>290 295 300     | 912  |
| TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT<br>Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His<br>305 310 315 320 | 960  |
| CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG<br>Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala<br>325 330 335     | 1008 |
| ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG<br>Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val<br>340 345 350     | 1056 |
| GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG<br>Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro<br>355 360 365     | 1104 |
| GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T<br>Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu<br>370 375 380   | 1153 |
| GA  | 1155 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser  
1 5 10 15

Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr  
20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser  
50 55 60

Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  
65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His  
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
145 150 155 160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
165 170 175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu  
180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg  
195 200 205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu  
210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
225 230 235 240

Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr  
245 250 255

Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr  
260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp  
275 280 285

Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile  
290 295 300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
305 310 315 320

Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala  
325 330 335

Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val  
340 345 350

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro  
355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu  
370 375 380

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Brassica napus

(vii) IMMEDIATE SOURCE:

(B) CLONE: IMC129

(ix) FEATURE:

(D) OTHER INFORMATION: T to A transversion  
mutation at nucleotide 515 of the F form.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT 48  
Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser  
1 5 10 15

GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT 96  
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr  
20 25 30

GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG 144  
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
35 40 45

ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC 192  
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser  
50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGC | TTC | TAC | TAC | NTC | GCC | ACC | ACT | TAC | TTC | CCT | CTC | CTC | CCT | CAC | CCT | 240 |
| Cys | Phe | Tyr | Tyr | Xaa | Ala | Thr | Thr | Tyr | Phe | Pro | Leu | Leu | Pro | His | Pro |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| CTC | TCC | TAC | TTC | GCC | TGG | CCT | CTC | TAC | TGG | GCC | TGC | CAA | GGG | TGC | GTC | 288 |
| Leu | Ser | Tyr | Phe | Ala | Trp | Pro | Leu | Tyr | Trp | Ala | Cys | Gln | Gly | Cys | Val |     |
| 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |     |     |     |     |
| CTA | ACC | GGC | GTC | TGG | GTC | ATA | GCC | CAC | GAG | TGC | GGC | CAC | CAC | GCC | TTC | 336 |
| Leu | Thr | Gly | Val | Trp | Val | Ile | Ala | His | Glu | Cys | Gly | His | His | Ala | Phe |     |
| 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |     |
| AGC | GAC | TAC | CAG | TGG | CTT | GAC | GAC | ACC | GTC | GGT | CTC | ATC | TTC | CAC | TCC | 384 |
| Ser | Asp | Tyr | Gln | Trp | Leu | Asp | Asp | Thr | Val | Gly | Leu | Ile | Phe | His | Ser |     |
| 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |
| TTC | CTC | CTC | GTC | CCT | TAC | TTC | TCC | TGG | AAG | TAC | AGT | CAT | CGC | AGC | CAC | 432 |
| Phe | Leu | Leu | Val | Pro | Tyr | Phe | Ser | Trp | Lys | Tyr | Ser | His | Arg | Ser | His |     |
| 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |     |
| CAT | TCC | AAC | ACT | GGC | TCC | CTC | GAG | AGA | GAC | GAA | GTG | TTT | GTC | CCC | AAG | 480 |
| His | Ser | Asn | Thr | Gly | Ser | Leu | Glu | Arg | Asp | Glu | Val | Phe | Val | Pro | Lys |     |
| 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |     |     |
| AAG | AAG | TCA | GAC | ATC | AAG | TGG | TAC | GGC | AAG | TAC | CTC | AAC | AAC | CCT | TTG | 528 |
| Lys | Lys | Ser | Asp | Ile | Lys | Trp | Tyr | Gly | Lys | Tyr | Leu | Asn | Asn | Pro | Leu |     |
| 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |     |     |     |     |
| GGA | CGC | ACC | GTG | ATG | TTA | ACG | GTT | CAG | TTC | ACT | CAC | GGC | TGG | CCG | TTG | 576 |
| Gly | Arg | Thr | Val | Met | Leu | Thr | Val | Gln | Phe | Thr | His | Gly | Trp | Pro | Leu |     |
| 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |     |     |     |
| TAC | TTA | GCC | TTC | AAC | GTC | TCG | GGA | AGA | CCT | TAC | GAC | GGC | GGC | TTC | CGT | 624 |
| Tyr | Leu | Ala | Phe | Asn | Val | Ser | Gly | Arg | Pro | Tyr | Asp | Gly | Gly | Phe | Arg |     |
| 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |     |     |
| TGC | CAT | TTC | CAC | CCC | AAC | GCT | CCC | ATC | TAC | AAC | GAC | CGC | GAG | CGT | CTC | 672 |
| Cys | His | Phe | His | Pro | Asn | Ala | Pro | Ile | Tyr | Asn | Asp | Arg | Glu | Arg | Leu |     |
| 210 |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |     |
| CAG | ATA | TAC | ATC | TCC | GAC | GCT | GGC | ATC | CTC | GCC | GTC | TGC | TAC | GGT | CTC | 720 |
| Gln | Ile | Tyr | Ile | Ser | Asp | Ala | Gly | Ile | Leu | Ala | Val | Cys | Tyr | Gly | Leu |     |
| 225 |     |     |     |     |     | 230 |     |     |     | 235 |     |     | 240 |     |     |     |
| TTC | CGT | TAC | GCC | GCC | GGC | CAG | GGA | GTG | GCC | TCG | ATG | GTC | TGC | TTC | TAC | 768 |
| Phe | Arg | Tyr | Ala | Ala | Gly | Gln | Gly | Val | Ala | Ser | Met | Val | Cys | Phe | Tyr |     |
| 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |     |     |     |     |
| GGA | GTC | CCG | CTT | CTG | ATT | GTC | AAT | GGT | TTC | CTC | GTG | TTG | ATC | ACT | TAC | 816 |
| Gly | Val | Pro | Leu | Leu | Ile | Val | Asn | Gly | Phe | Leu | Val | Leu | Ile | Thr | Tyr |     |
| 260 |     |     |     |     |     | 265 |     |     |     | 270 |     |     |     |     |     |     |
| TTG | CAG | CAC | ACG | CAT | CCT | TCC | CTG | CCT | CAC | TAC | GAT | TCG | TCC | GAG | TGG | 864 |
| Leu | Gln | His | Thr | His | Pro | Ser | Leu | Pro | His | Tyr | Asp | Ser | Ser | Glu | Trp |     |
| 275 |     |     |     |     |     | 280 |     |     |     | 285 |     |     |     |     |     |     |
| GAT | TGG | TTC | AGG | GGA | GCT | TTG | GCT | ACC | GTT | GAC | AGA | GAC | TAC | GGA | ATC | 912 |
| Asp | Trp | Phe | Arg | Gly | Ala | Leu | Ala | Thr | Val | Asp | Arg | Asp | Tyr | Gly | Ile |     |
| 290 |     |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |     |

|   |      |
|---|------|
| TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT   | 960  |
| Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His   |      |
| 305 310 315 320   |      |
| CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG   | 1008 |
| Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala   |      |
| 325 330 335   |      |
| ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG   | 1056 |
| Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val   |      |
| 340 345 350   |      |
| GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG   | 1104 |
| Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro   |      |
| 355 360 365   |      |
| GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T | 1153 |
| Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu   |      |
| 370 375 380   |      |
| GA  | 1155 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|   |  |
|---|--|
| Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser |  |
| 1 5 10 15   |  |
| Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr |  |
| 20 25 30  |  |
| Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser |  |
| 35 40 45  |  |
| Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser |  |
| 50 55 60  |  |
| Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro |  |
| 65 70 75 80   |  |
| Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val |  |
| 85 90 95  |  |
| Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe |  |
| 100 105 110   |  |
| Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser |  |
| 115 120 125   |  |
| Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His |  |
| 130 135 140   |  |

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150 155 160  
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu  
 165 170 175  
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg  
 195 200 205  
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu  
 210 215 220  
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
 225 230 235 240  
 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr  
 245 250 255  
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr  
 260 265 270  
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp  
 275 280 285  
 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile  
 290 295 300  
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
 305 310 315 320  
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala  
 325 330 335  
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val  
 340 345 350  
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro  
 355 360 365  
 Asp Arg Gln Gly Glu Lys Lys Gly val Phe Trp Tyr Asn Asn Lys Leu  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1155 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Brassica napus

## (ix) FEATURE:

(D) OTHER INFORMATION: Wild type D form.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|   |     |
|---|-----|
| ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT | 48  |
| Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser |     |
| 1 5 10 15   |     |
| GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT | 96  |
| Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr |     |
| 20 25 30  |     |
| GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG | 144 |
| Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser |     |
| 35 40 45  |     |
| ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC | 192 |
| Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser |     |
| 50 55 60  |     |
| TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT | 240 |
| Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro |     |
| 65 70 75 80   |     |
| CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG GGC TGC GTC | 288 |
| Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val |     |
| 85 90 95  |     |
| CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC CAC GCC TTC | 336 |
| Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe |     |
| 100 105 110   |     |
| AGC GAC TAC CAG TGG CTG GAC ACC GTC GGC CTC ATC TTC CAC TCC     | 384 |
| Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser |     |
| 115 120 125   |     |
| TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGA CGC CAC | 432 |
| Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His |     |
| 130 135 140   |     |
| CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG | 480 |
| His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys |     |
| 145 150 155 160   |     |
| AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG | 528 |
| Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu |     |
| 165 170 175   |     |
| GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG | 576 |
| Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu |     |
| 180 185 190   |     |
| TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT | 624 |
| Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala |     |
| 195 200 205   |     |
| TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC | 672 |
| Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu |     |
| 210 215 220   |     |

|   |      |
|---|------|
| CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC<br>Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu<br>225 230 235 240 | 720  |
| TAC CGC TAC GCT GTC CAA GGA GTT GCC TCG ATG GTC TGC TTC TAC<br>Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr<br>245 250 255         | 768  |
| GGA GTT CCG CTT CTG ATT GTC AAT GGG TTC TTA GTT TTG ATC ACT TAC<br>Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr<br>260 265 270     | 816  |
| TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG TCT GAG TGG<br>Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp<br>275 280 285     | 864  |
| GAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC TAC GGA ATC<br>Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile<br>290 295 300     | 912  |
| TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG GCG CAT CAC<br>Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His<br>305 310 315 320 | 960  |
| CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT ACG AAG GCG<br>Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala<br>325 330 335     | 1008 |
| ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTG CAT GGG ACG CCG GTG<br>Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val<br>340 345 350     | 1056 |
| GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG<br>Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro<br>355 360 365     | 1104 |
| GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T<br>Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu<br>370 375 380   | 1153 |
| GA  | 1155 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|  |
|--|
| Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser<br>1 5 10 15 |
| Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr<br>20 25 30  |
| Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser<br>35 40 45  |

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser  
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  
65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
145 150 155 160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
165 170 175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu  
180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala  
195 200 205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu  
210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
225 230 235 240

Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr  
245 250 255

Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr  
260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp  
275 280 285

Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile  
290 295 300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
305 310 315 320

Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala  
325 330 335

Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val  
340 345 350

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro  
355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu  
370 375 380

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Brassica napus

(vii) IMMEDIATE SOURCE:

(B) CLONE: Q508

(ix) FEATURE:

(D) OTHER INFORMATION: G to A transversion mutation at nucleotide 316 of the D form.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|   |     |
|---|-----|
| ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT | 48  |
| Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser |     |
| 1 5 10 15   |     |
| GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT | 96  |
| Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr |     |
| 20 25 30  |     |
| GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG | 144 |
| Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser |     |
| 35 40 45  |     |
| ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC | 192 |
| Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser |     |
| 50 55 60  |     |
| TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT | 240 |
| Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro |     |
| 65 70 75 80   |     |
| CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG GGC TGC GTC | 288 |
| Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val |     |
| 85 90 95  |     |
| CTA ACC GGC GTC TGG GTC ATA GCC CAC AAG TGC GGC CAC CAC GCC TTC | 336 |
| Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe |     |
| 100 105 110   |     |
| AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC | 384 |
| Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser |     |
| 115 120 125   |     |
| TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGA CGC CAC | 432 |
| Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His |     |
| 130 135 140   |     |

|   |  |      |
|---|--|------|
| CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG   |  | 480  |
| His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys   |  |      |
| 145 150 155 160   |  |      |
| AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG   |  | 528  |
| Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu   |  |      |
| 165 170 175   |  |      |
| GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG   |  | 576  |
| Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu   |  |      |
| 180 185 190   |  |      |
| TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT   |  | 624  |
| Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala   |  |      |
| 195 200 205   |  |      |
| TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC   |  | 672  |
| Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu   |  |      |
| 210 215 220   |  |      |
| CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC   |  | 720  |
| Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu   |  |      |
| 225 230 235 240   |  |      |
| TAC CGC TAC GCT GTC CAA GGA GTT GCC TCG ATG GTC TGC TTC TAC       |  | 768  |
| Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr   |  |      |
| 245 250 255   |  |      |
| GGA GTT CCG CTT CTG ATT GTC AAT GGG TTC TTA GTT TTG ATC ACT TAC   |  | 816  |
| Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr   |  |      |
| 260 265 270   |  |      |
| TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG TCT GAG TGG   |  | 864  |
| Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp   |  |      |
| 275 280 285   |  |      |
| GAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC TAC GGA ATC   |  | 912  |
| Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile   |  |      |
| 290 295 300   |  |      |
| TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG GCG CAT CAC   |  | 960  |
| Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His   |  |      |
| 305 310 315 320   |  |      |
| CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT ACG AAG GCG   |  | 1008 |
| Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala   |  |      |
| 325 330 335   |  |      |
| ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTG CAT GGG ACG CCG GTG   |  | 1056 |
| Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val   |  |      |
| 340 345 350   |  |      |
| GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG   |  | 1104 |
| Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro   |  |      |
| 355 360 365   |  |      |
| GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T |  | 1153 |
| Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu   |  |      |
| 370 375 380   |  |      |
| GA  |  | 1155 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser  
1 5 10 15

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr  
20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser  
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  
65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe  
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
145 150 155 160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
165 170 175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu  
180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala  
195 200 205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu  
210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
225 230 235 240

Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr  
245 250 255

Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr  
260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp  
275 280 285

Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile  
290 295 300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
305 310 315 320

Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala  
325 330 335

Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val  
340 345 350

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro  
355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu  
370 375 380